Sequence Alignments

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                    GenCore version 5.1.3
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QM nucleic - nucleic search, using sw model

Run on:         January 6, 2003, 13:55:36 ; Search time 58 seconds
                                (without alignments)
                                6062.518 Million cell updates/sec

Title:          US-09-936-024-2
Perfect score:  813
Sequence:       1 gtcggcagaaacacccaccta.........agcgcttcctccctgtgcac 813

Scoring table:  IDENTITY_NUC
                Gapop 10.0 , Gapext 1.0

Searched:       381593 seqs, 216252194 residues

Total number of hits satisfying chosen parameters:       763186

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

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pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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Result        Query
No.   Score   Match  Length  DB  ID                     Description
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  1   813    100.0   1077    10  US-09-935-727-1         Sequence  1, Appli
  2   813    100.0   1114    10  US-09-896-096A-2        Sequence  2, Appli
  3   813    100.0   1114    10  US-09-894-924-2         Sequence  6, Appli
  4   813    100.0   1347    10  US-09-877-156-18        Sequence 18, Appl
  5   803.4   99.9   1859    10  US-09-877-155-19        Sequence 19, Appl
  6   533.4   65.6    903    10  US-09-935-727-32        Sequence 32, Appl
  7   515.4   63.4    491    10  US-09-896-096A-3        Sequence  3, Appli
  8   473.4   58.2    491    10  US-09-894-924-3         Sequence  3, Appli
  9   473.4   58.2    491    10  US-09-877-156-7         Sequence  7, Appli
 10   459    56.5    459    10  US-09-894-924-3         Sequence  3, Appli
 11   392.2   48.2   1550    10  US-09-935-727-33        Sequence 33, Appl
 12   387    47.6   1667    10  US-09-935-727-28        Sequence 28, Appl
 13   387    47.6   1796    10  US-09-935-727-28        Sequence 28, Appl
 14   245.2   30.2    271    10  US-09-896-096A-10       Sequence 10, Appl
 15   245.2   30.2    271    10  US-09-894-924-5         Sequence  5, Appli
 16   242.2   29.8    271    10  US-09-894-924-10        Sequence 10, Appl
 17   242.2   29.8    283    10  US-09-935-727-17        Sequence 17, Appl
 18   242.2   29.8    283    10  US-09-896-096A-9        Sequence  9, Appli
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 22   200     24.6    201    10  US-09-894-924-6         Sequence  6, Appli
 23   194.2   23.9    199    10  US-09-896-096A-8        Sequence  8, Appli
 24   194.2   23.9    199    10  US-09-894-924-8         Sequence  8, Appli
 25   183     22.5    233    10  US-09-292-758-141       Sequence 141, App
 26   152.2   18.7    277    10  US-09-896-096A-17       Sequence 18, Appl
 27   152.2   18.7    277    10  US-09-894-924-7         Sequence  7, Appli
 28   103.4   12.7    277    10  US-09-896-096A-7        Sequence  7, Appli
 29   103     12.7    564    10  US-09-062-113-102       Sequence 102, App
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 31   103     12.7    819    10  US-09-062-113-96        Sequence 96, Appl
 32   103     12.7    986    10  US-09-062-113-101       Sequence 101, App
 33   103     12.7    984    10  US-09-062-113-92        Sequence 92, Appl
 34   103     12.7    984    10  US-09-062-113-93        Sequence 93, Appl
 35   103     12.7   1056    10  US-09-062-113-95        Sequence 95, Appl
 36   103     12.7   1089    10  US-09-062-113-10        Sequence 10, Appl
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 39   103     12.7   1203    10  US-10-105-934-3         Sequence  3, Appli
 40   103     12.7   1203    12  US-09-062-113-6         Sequence  6, Appli
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 44   103     12.7   1206    10  US-09-062-113-86        Sequence 86, Appl
 45   103     12.7   1206    10  US-09-062-113-87        Sequence 87, Appl
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ALIGNMENTS

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;   LOCATION: (25)..(924)
US-09-935-727-1

Query Match        100.0%;  Score 813;  DB 10;  Length 1077;
Best Local Similarity  100.0%;  Pred. No. 7.8e-162;
Matches  813;  Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;

Qy     1  GTGGCAGAAACACCACCTACCCCTGGCGGGACCAGAGACAGGGGGACCGGCTGGTGTGC    60
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Db   592  GACACCCGTGTGCACCAGCTGCACCGCGTGGCTTCCCCCTCAGCACCAGGGAGGACTCAGCG   651

Qy   541  GAGTGTGCAGGCCGCGTCATCGACTTGTGGCTTTCCAGGACATCATCCATCCAAGAGGCTG   600
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RESULT 2
US-09-896-096A-2
; Sequence 2, Application US/09896096A
; Patent No. US2002006155pAl
; GENERAL INFORMATION:
>   APPLICANT: ASHKENAZI, AVI J
>   APPLICANT: BOTSTEIN, DAVID
>   APPLICANT: DODGE, KELLY H.
>   APPLICANT: GURNEY, AUSTIN L.

```
;   APPLICANT:  KIM, KYUNG JIN
;   APPLICANT:  LAWRENCE, DAVID A.
;   APPLICANT:  PITTI, ROBERT
;   APPLICANT:  ROY, MARGARET A
;   APPLICANT:  TUMAS, DANIEL B
;   APPLICANT:  WOOD, WILLIAM I.
;   TITLE OF INVENTION: DcR3 Polypeptide, A TNFR Homolog
;   FILE REFERENCE: P1134R2 REVISED
    CURRENT APPLICATION NUMBER: US 09/896,096A
    CURRENT FILING DATE: 2001-06-28
    PRIOR APPLICATION NUMBER: US 09/157,289
    PRIOR FILING DATE: 1998-09-18
    PRIOR APPLICATION NUMBER: US 60/059,288
    PRIOR FILING DATE: 1997-09-18
    PRIOR APPLICATION NUMBER: US 60/094,640
    PRIOR FILING DATE: 1998-07-30
    NUMBER OF SEQ ID NOS: 18
    SEQ ID NO 2
    LENGTH: 1114
    TYPE: DNA
    ORGANISM: Homo sapiens
    FEATURE:
    NAME/KEY: Unsure
    LOCATION: 1090
    OTHER INFORMATION: Unknown base
US-09-896-096A-2

Query Match        100.0%;  Score 813;  DB 10;  Length 1114;
Best Local Similarity  100.0%;  Pred. No. 7.8e-162;
Matches  813;  Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;

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Qy   601  CAGCGGCTGCTGCAGGCCCGCTGCAGGCGCTGGGGTCCGACACCAAGGGCGGCTG   660
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Db   601  CAGCGGCTGCTGCAGGCCCGCTGCAGGCGCTGGGGTCCGACACCAAGGGCGGCTG   660
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                    GenCore version 5.1.3
          Copyright (c) 1993 - 2003 Compugen Ltd.

QM nucleic - nucleic search, using aw model

Run on:        January 6, 2003, 13:48:11 ; Search time 54 seconds
                                          [without alignments]
                                          4617.189 Million cell updates/sec

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Perfect score: 813
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Scoring table: IDENTITY.NUC
               GapOp 10.0 , GapExt 1.0

Searched:      441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters:     882724

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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SUMMARIES

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1	813	100.0	2	1164	US-08-794-796-1	Sequence 1, Appli
2	813	100.0	4	1347	US-09-286-529-18	Sequence 18, Appl
3	533.4	65.6	4	1859	US-09-286-529-19	Sequence 19, Appl
4	459	56.5	4	459	US-09-286-529-7	Sequence 7, Appl
5	127.6	15.8	2	2435	US-08-937-912-1	Sequence 47, Appl
6	112	13.8	3	2432	US-08-795-447A-1	Sequence 1, Appl
7	112	13.8	3	2432	US-08-795-445A-1	Sequence 1, Appl
8	112	13.8	3	2432	US-08-795-147A-1	Sequence 1, Appli
9	112	13.8	3	2432	US-08-974-186-1	Sequence 1, Appl
10	112	13.8	2	2432	US-08-795-446B-1	Sequence 1, Appl
11	112	13.6	3	1324	US-08-795-445B-123	Sequence 123, App
12	110.4	13.6	3	1324	US-08-974-022-3	Sequence 3, Appli
13	110.4	13.6	3	1324	US-08-795-445A-3	Sequence 3, Appl
14	110.4	13.6	3	1324	US-08-795-447A-3	Sequence 3, Appl
15	110.4	13.6	3	1324	US-08-974-186-3	Sequence 3, Appl
16	110.4	13.6	3	1324	US-08-795-446B-3	Sequence 3, Appl
17	110.4	13.6	3	1354	US-08-706-795D-125	Sequence 125, App
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20	103	12.7	4	1355	US-08-795-447A-5	Sequence 5, Appl
21	103	12.7	4	1355	US-08-974-186-5	Sequence 5, Appl
22	103	12.7	4	1355	US-08-795-446B-5	Sequence 5, Appl
23	103	12.7	4	1355	US-08-706-795D-127	Sequence 127, App
24	68	8.4	3	759	US-09-042-785A-6	Sequence 6, Appl
25	68	8.4	4	1015	US-09-042-785A-24	Sequence 24, Appl
26	68	8.4	4	2186	US-08-959-382-1	Sequence 1, Appli
27						

28	68	8.4	2612	4	US-09-042-785A-3	Sequence 3, Appl
29	68	8.4	2610	4	US-09-043-785A-22	Sequence 22, Appl
30	56.4	6.9	3474	4	US-09-527-236A-1	Sequence 1, Appl
31	54.8	6.7	1719	4	US-09-042-785A-5	Sequence 5, Appl
32	54.8	6.7	1164	2	US-08-794-796-1	Sequence 18, Appl
33	52	6.4	1347	4	US-09-286-529-18	Sequence 18, Appl
34	52	6.4	2793	1	US-08-209-747-1	Sequence 1, Appl
35	51.6	6.3	3796	2	US-08-762-308-11	Sequence 11, Appl
36	51.6	6.3	3796	4	US-09-844-634-10	Sequence 10, Appl
37	51.6	6.3	3813	6	US-08-650-000-3	Sequence 3, Appl
38	51.6	6.3	3813	6	5395760-3	Patent No. 5395760
39	49.6	6.1	691	1	US-08-266-0808-12	Sequence 12, Appl
40	49.6	6.1	691	5	US-09-527-236A-12	Sequence 12, Appl
42	49.4	6.0	705	4	US-09-336-394-3	Sequence 3, Appl
43	49.4	6.0	8906	2	US-08-826-267-1	Sequence 1, Appl
44	48.6	6.0	1878	3	US-08-996-139-14	Sequence 14, Appl
45	48.6	6.0	1878	4	US-08-995-659-14	Sequence 14, Appl

Matches 813; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy     61  GCCCAGTGCCCCCCAGGCACTTTGTGCAGCGGCCGTGCCCGAGACAGCCCCACGACG  120
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Qy    121  TGTGGCCCGGTGTCCACCGGCCCACTACACGCAGTTCTGGAACTACCTGGAGGCGTGC  180
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Db    318  TGTGGCCCGGTGTCCACCGGCCCACTACACGCAGTTCTGGAACTACCTGGAGGCGTGC  377

Qy    181  TACTGCAACGTCCTCTCGCGGGGGACGTCAGGAGGCACGGCTTGCCACGCCACCCAC  240
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Qy    541  GAGTGTGAGGCGTGCCGTCATTCCATCTTTCCAGGACATCTCCATCCAACCAGACGCTGG  600
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    738  GAGTGTGAGGCGTGCCGTCATTCCATCTTTCCAGGACATCTCCATCCAACCAGACGCTGG  797

Qy    601  CAGCCGGCTTCGCCTCGAGGCCCCTCGAGGCCCGGAGGCGTGGGGTCGGACACCAAGGCGGGC  660
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    798  CAGCCGGCTTCGCCTCGAGGCCCCTCGAGGCCCGGAGGCGTGGGGTCGGACACCAAGGCGGGC  857

Qy    661  CGCGCCGGCCTTGCACTGCGAGCTGTCGCCTCGGCGTGCTCACGGGAGCTCCTCGGGGCGGAC  720
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    858  CGCGCCGGCCTTGCACTGCGAGCTGTCGCCTCGGCGTGCTCACGGGAGCTCCTCGGGGCGGAC  917

Qy    721  GGGGCGGCCTTGCGGTCGCGGCTGCTCAGCCGCTGGCGGCGGTGGCCAGGATCGCCGGCTGAG  780
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    918  GGGGCGGCCTTGCGGTCGCGGCTGCTCAGCCGCTGGCGGCGGTGGCCAGGATCGCCGGCTGAG  977

Qy    781  CGGAGCGTCCGTGAGCGGCGTCCTCCCTGTGCAC  813
           ||||||||||||||||||||||||||||||||||
Db    978  CGGAGCGTCCGTGAGCGGCGTCCTCCCTGTGCAC  1010
```

RESULT 2
US-09-286-529-18
; Sequence 18, Application US/09286529
; Patent No. 6297367;
; GENERAL INFORMATION.
; APPLICANT: Catherine Tribouley
; TITLE OF INVENTION: NEW MEMBERS OF TNF AND TNFR FAMILIES
; FILE REFERENCE: 1408.003/200130.439C1
; CURRENT APPLICATION NUMBER: US/09/286,529
; CURRENT FILING DATE: 1999-04-05
; NUMBER OF SEQ ID NOS: 25
; SEQ ID NO 18
; FastSEQ for Windows Version 3.0
; SEQ ID NO 18
; LENGTH: 1347

; TYPE: DNA
; ORGANISM: Homo sapien
US-09-286-529-18

Query Match   100.0%; Score 813; DB 4; Length 1347;
Best Local Similarity 100.0%; Pred. No. 2.6e-154;
Matches 813; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy      1  GTGGCAGAAACACCAACTACCCCTGGCGGACCGAGAGAGGGGAGCGGCGTGGTGTGC   60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    405  GTGGCAGAAACACCAACTACCCCTGGCGGACCGAGAGAGGGGAGCGGCGTGGTGTGC  464

Qy     61  GCCCAGTGCCCCCCAGGCACTTTGTGCAGCGGCCGTGCCCGAGACAGCCCCACGACG  120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    465  GCCCAGTGCCCCCCAGGCACTTTGTGCAGCGGCCGTGCCCGAGACAGCCCCACGACG  524

Qy    121  TGTGGCCCGGTGTCCACCGGCCCACTACACGCAGTTCTGGAACTACCTGGAGGCGTGC  180
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    525  TGTGGCCCGGTGTCCACCGGCCCACTACACGCAGTTCTGGAACTACCTGGAGGCGTGC  584

Qy    181  TACTGCAACGTCCTCTCGCGGGGGACGTCAGGAGGCACGGCTTGCCACGCCACCCAC  240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    585  TACTGCAACGTCCTCTCGCGGGGGACGTCAGGAGGCACGGCTTGCCACGCCACCCAC  644

Qy    241  AACCGGTGCCTGCCCGCACCGGCTTCCTCGGCCAGCTGGTTTCTGCTTGGAGCAC  300
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    645  AACCGGTGCCTGCCCGCACCGGCTTCCTCGGCCAGCTGGTTTCTGCTTGGAGCAC  704

Qy    301  GCATCGTGTCCAACCTGGTGCCGGCGTGATTGCCCCGGCCAGACCAGACACGCAG  360
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    705  GCATCGTGTCCAACCTGGTGCCGGCGTGATTGCCCCGGCCAGACCAGACACGCAG  764

Qy    361  TGCCAGCCGTGCCCCCAGGCACTTCTCAGCAAGCAGCTCAGCTCAGAGCAGTGCCAG  420
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    765  TGCCAGCCGTGCCCCCAGGCACTTCTCAGCAAGCAGCTCAGCTCAGAGCAGTGCCAG  824

Qy    421  CCCCACCGGCACTGCACGGCCCTGGGCCTGGCCCTCAATGTGCCAGGCTCTTCCTCCCAT  480
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    825  CCCCACCGGCACTGCACGGCCCTGGGCCTGGCCCTCAATGTGCCAGGCTCTTCCTCCCAT  884

Qy    481  GACACCCCGGCACCAGCTGCACGGCTGGCTTCCCCCTCAGCACCAGGGTACCAGGAGCTGAG  540
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    885  GACACCCCGGCACCAGCTGCACGGCTGGCTTCCCCCTCAGCACCAGGGTACCAGGAGCTGAG  944

Qy    541  GAGTGTGAGGCGTGCCGTCATTGCACTTTGTGCCTTTCCAGGACATCTCCATCCAAGGAGGCTG  600
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    945  GAGTGTGAGGCGTGCCGTCATTGCACTTTGTGCCTTTCCAGGACATCTCCATCCAAGGAGGCTG  1004

Qy    601  CAGCGGCGTGCTGCAGGCCCTCGAGGCCCGGAGGCGTGGGGTCGGACACCAAGGGCGGGC  660
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1005  CAGCGGCGTGCTGCAGGCCCTCGAGGCCCGGAGGCGTGGGGTCGGACACCAAGGGCGGGC  1064

Qy    661  CGCGCCGGCCTTGCAGCTGAAGCTGGCTCGGTCGGCCTCACGGAGCTTCTGGGGGCGGACGGAC  720
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1065  CGCGCCGGCCTTGCAGCTGAAGCTGGCTCGGTCGGCCTCACGGAGCTTCTGGGGGCGGACGGAC  1124

Qy    721  GGGGCGGCTTGCTGGTGCGCGTGCTGCAGGCGGCTGCAGGGCAGGAGTGCCGGGGCTGCAG  780
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1125  GGGGCGGCTTGCTGGTGCGCGTGCTGCAGGCGGCTGCAGGGCAGGAGTGCCGGGGCTGCAG  1184

Qy    781  CGGAGCGTCCGTGAGCGGCGTCCTCCCTGTGCAC  813
           ||||||||||||||||||||||||||||||||||
Db   1185  CGGAGCGTCCGTGAGCGGCGTCCTCCCTGTGCAC  1217
```

RESULT 3
US-09-286-529-19
; Sequence 19, Application US/09286529
; Patent No. 6297367;
; GENERAL INFORMATION.
; APPLICANT: Catherine Tribouley
; TITLE OF INVENTION: NEW MEMBERS OF TNF AND TNFR FAMILIES
; FILE REFERENCE: 1408.003/200130.439C1

CC particularly of the immune system, substantially altered (whether
CC increased or decreased) levels of TNFR-6 alpha and/or TNFR-6 beta gene
CC expression can be detected therefore the TNFR-6 alpha and/or TNFR-6 beta
CC polypeptides, nucleic acids and antibodies are claimed to be useful in
CC the diagnosis of such disorders. Mutations of the TNFR-6 alpha and
CC TNFR-6 beta genes can also be detected. The TNFR polypeptides are
XX also claimed to be useful for identifying ligands which may be useful
XX in the treatment of apoptosis related disorders.
SQ Sequence 1077 BP; 196 A; 360 C; 326 G; 195 T; 0 other;

```
Query Match       100.0%;  Score 813;  DB 19;  Length 1077;
Best Local Similarity  100.0%;  Pred. No. 5.1e-145;
Matches 813;  Conservative   0;  Mismatches   0;  Indels   0;  Gaps   0;

Qy     1 GTGGCAGAAACACCCACCTACCCC......GACG    60
         ||||||||||||||||||||||||||||||||||||
Db   112 GTGGCAGAAACACCCACCTACCCC......GACG   171

Qy    61 GCCCAGGTGCCCCCAGGCACCTT...CCCACGACG   120
         ||||||||||||||||||||||||||||||||||||
Db   172 GCCCAGGTGCCCCCAGGCACCTT...CCCACGACG   231

Qy   121 TGTGGCCCGTGTCACCGGCGCACT...GCCTGCCGC   180
         ||||||||||||||||||||||||||||||||||||
Db   232 TGTGGCCCGTGTCACCGGCGCACT...GCCTGCCGC   291

Qy   181 TACTGCGAACGTCCTGTGGGGAGC...GCCACCCAC   240
         ||||||||||||||||||||||||||||||||||||
Db   292 TACTGCGAACGTCCTGTGGGGAGC...GCCACCCAC   351

Qy   241 AACCGTGCCTGCCCGTGCCCCACC...CTGCACGGAG   300
         ||||||||||||||||||||||||||||||||||||
Db   352 AACCGTGCCTGCCCGTGCCCCACC...CTGCACGGAG   411

Qy   301 GCATCGTGTCCACCTGGTGCGCCG...CCACGCAG   360
         ||||||||||||||||||||||||||||||||||||
Db   412 GCATCGTGTCCACCTGGTGCGCCG...CCACGCAG   471

Qy   361 TGCCAGGCTGCCCCCCAGGCACCT...CAGTGCCAG   420
         ||||||||||||||||||||||||||||||||||||
Db   472 TGCCAGGCTGCCCCCCAGGCACCT...CAGTGCCAG   531

Qy   421 CCCCACCGCAACTGCACGGCCCTG...TTCCTCCCAT   480
         ||||||||||||||||||||||||||||||||||||
Db   532 CCCCACCGCAACTGCACGGCCCTG...TTCCTCCCAT   591

Qy   481 GACACCCTGTGCAGGCAGCTGCAC...GCAGGAGCTGAG   540
         ||||||||||||||||||||||||||||||||||||
Db   592 GACACCCTGTGCAGCCAGCTGCAC...GCAGGAGCTGAG   651

Qy   541 GAGTGTGAGCGTGCCCGTCATCGA...CATCAAGAGGCTG   600
         ||||||||||||||||||||||||||||||||||||
Db   652 GAGTGTGAGCGTGCCCGTCATCGA...CATCAAGAGGCTG   711

Qy   601 CAGCGGGCTGCTGCAGGCCCTGGAG...CAACAAGGGCGGGC   660
         ||||||||||||||||||||||||||||||||||||
Db   712 CAGCGGGCTGCTGCAGGCCCTGGAG...CAACAAGGGCGGGCC   771

Qy   661 CGCGCGGGCCTTGCAGCTGGAGTC...GCGGGGCCCAGGAC   720
         ||||||||||||||||||||||||||||||||||||
Db   772 CGCGCGGGCCTTGCAGCTGGAGTC...GCGGGGCCCAGGAC   831

Qy   721 GGGGCGTGCTGGTGCGGCTGCTGCAGG...CGGGCTGGAG   780
         ||||||||||||||||||||||||||||||||||||
Db   832 GGGGCGTGCTGGTGCGGCTGCTGCAGG...CGGGCTGGAG   891

Qy   781 CCGAGCCTCCGTGAGCGCTTCCCTGTGCAC   813
         ||||||||||||||||||||||||||||||
Db   892 CGGAGCCTCCGTGAGCGCTTCTCCTGTGCAC   924
```

RESULT 14

```
Qy   541 GAGTGTGAGCGTGCCCGTCATCGACGTTTGTGGCTTTCCAGGACATCTCCATCAAGAGGCTG   600
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   680 GAGTGTGAGCGTGCCCGTCATCGACGTTTGTGGCTTTCCAGGACATCTCCATCAAGAGGCTG   739

Qy   601 CAGCGGGCTGCTGCAGGCCCTGGAGGGGTGGGGGTTCGGACAACCAAGGGCGGGC   660
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   740 CAGCGGGCTGCTGCAGGCCCTGGAGGGGTGGGGGTTCGGACAACCAAGGGCGGGCC   799

Qy   661 CGCGCGGGCCTTGCAGCTGGAGTCGCGTCGGCGGCGGCTCACGGGAGCCCAGGAC   720
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   800 CGCGCGGGCCTTGCAGCTGGAGTCGCGTCGGCGGCGGCTCACGGGAGCCCAGGAC   859

Qy   721 GGGGCGTGCTGGTGCGGCTGCTGCAGGATGCCCGGGCTGGAG   780
         ||||||||||||||||||||||||||||||||||||||||||
Db   860 GGGGCGTGCTGGTGCGGCTGCTGCAGGATCCCGGGCTGGAG   919

Qy   781 CCGAGCCTCCGTGAGCGCTTCCCTGTGCAC   813
         ||||||||||||||||||||||||||||||
Db   920 CGGAGCCTCCGTGAGCGCTTCTCCTGTGCAC   952
```

RESULT 13
AAV39085
ID AAV39085 standard; cDNA; 1077 BP.
AC AAV39085;
XX
DT 26-OCT-1998 (first entry)
XX
DE Human tumour necrosis factor receptor-6 alpha cDNA.
XX
KW Human tumour necrosis factor receptor-6 alpha; TNFR-6 alpha; TNFR-6 beta;
KW endothelial cells; keratinocytes; normal prostate; apoptosis;
KW prostate tumour tissue; ss.
XX
OS Homo sapiens.
XX
FH Key   Location/Qualifiers
CDS   25..927
                /tags= a
                /product= "TNFR-6 alpha protein"
FT sig_peptide   25..114
FT   /tags= b
FT mat_peptide   115..924
FT   /tags= c
XX
PN WO9830694-A2.
XX
PD 16-JUL-1998.
XX
PF 13-JAN-1998; 98WO-US000153.
PR 14-JAN-1997; 97US-0035496.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Ebner R, Feng P, Gentz RL, Ni J, Ruben SM, Yu G;
XX
PT WPI; 1998-399142/34.
PT P-PSDB; AAW63622.
XX
PR Human tumour necrosis factor receptors 6-alpha and 6-beta - used in
PR the diagnosis of immune system-related disorder(s)
XX
PA Disclosure; Fig 1; 91pp; English.
XX
CC The present sequence represents the human tumour necrosis factor
CC receptor-6 alpha (TNFR-6 alpha) cDNA. The invention also provides
CC for the TNFR-6 beta cDNA (AAV39086). TNFR-6 alpha and TNFR-6 beta are
CC members of the tumour necrosis factor receptor (TNFR) family. TNFR6
CC are expressed in endothelial cells, keratinocytes, normal prostate and
CC prostate tumour tissue. For a number of disorders of these cells,

XX OS Homo sapiens.
XX RN W02001110908-A1.
XX PD 15-FEB-2001.
XX PF 02-AUG-2000; 2000MO-US211287.
XX PR 04-AUG-1999; 99US-0147297.
XX PA (AMGE-) AMGEN INC.
XX PI Hsu H;
XX PT WPI; 2001-191521/19.
XX DR P-PSDB; AAB71754.
PT New tumor necrosis factor receptor, NTR3, useful for treating cancers,
PT stroke, anemia, obesity, rheumatoid arthritis and transplantation
XX rejection -
PS
XX Claim 1; Page 128-129; 135pp; English.

CC The present sequence encodes the tumour necrosis factor (TNF) receptor
CC polypeptide NTR3. The NTR3 polynucleotides and polypeptides are useful
CC for treating diseases such as acquired-immunodeficiency syndrome (AIDS),
CC anaemia, autoimmune diseases, cachexia, cancer, cerebral malaria,
CC diabetes mellitus, disseminated intravascular coagulopathy, erythroid
CC sick syndrome, haemorrhagic shock, hepatitis, insulin resistance,
CC leprosy, leukaemia, meningitis, multiple sclerosis, myocardial ischaemia,
CC obesity, rejection of transplanted organs, rheumatoid arthritis, septic
CC shock syndrome, stroke, adult respiratory distress syndrome (ARDS),
CC tuberculosis, and a number of viral diseases. The NTR3 polypeptide is
CC useful for identifying or developing new (antagonists of NTR3. It may
CC be used as an immunogen to which antibodies may be raised. NTR3 nucleic
CC acid molecules may be useful as hybridisation probes in diagnostic assays
CC to test, either qualitatively or quantitatively, for the presence of an
CC NTR3 DNA or corresponding RNA in mammalian tissue or bodily fluid
XX samples.
SQ

SQ Sequence 1055 BP; 160 A; 369 C; 340 C; 186 T; 0 other;

Query Match   100.0%; Score 813; DB 22; Length 1055;
Best Local Similarity   100.0%; Pred. No. 5.1e-145;
Matches 813; Mismatches   0; Conservative   0; Indels   0; Gaps   0;

Qy   1 GTGGCAGAAACACCCACCTACCCCTGGCGGACGAGACAGGGAGCGCTGGTGTGC 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   154 GTGGCAGAAACACCCACCTACCCCTGGCGGACGAGACAGGGAGCGCTGGTGTGC 213

Qy   61 GCCCAGTGCCCCCAGGCACCTTGTGCAGCGGCCGGTGCCCGGAGCAGCCCACGACG 120
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   214 GCCCAGTGCCCCCAGGCACCTTGTGCAGCGGCCGGTGCCCGGAGCAGCCCACGACG 273

Qy   121 TGTGGCCCGTGTCCACCGGCGCCACTACAGCAGTTCTGGAACTACCTGGAGGCGCTGGCCGC 180
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   274 TGTGGCCCGTGTCCACCGGCGCCACTACAGCAGTTCTGGAACTACCTGGAGGCGCTGGCCGC 333

Qy   181 TACTGCAACGTCTCCTTGTCCGGGGAGCGTGAGGAGGAGCCGGGCCTTGCCAGGCCACCAC 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   334 TACTGCAACGTCTCCTTGTCCGGGGAGCGTGAGGAGGAGCCGGGCCTTGCCAGGCCACCAC 393

Qy   241 AACCGTGCCTGCGCGTGCCGCACGCGGCTTGTCCGGGGCACGCTGGTTCTGCTTGGAGCGAC 300
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   394 AACCGTGCCTGCGCGTGCCGCACGCGGCTTGTCCGGGGCACGCTGGTTCTGCTTGGAGCGAC 453

Qy   301 GCATCGTGTCCACCTGGTGCCCGAGGTGAGAGCGCACCCCGCAGAACACGCAG 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   454 GCATCGTGTCCACCTGGTGCCCGAGGTGAGAGCGCACCCCGCAGAACACGCAG 513

Qy   361 TGCCAGCCGTGCCCCCAGGATACCTTTCAGCCAGCAGCTTCAGAGCGTGCAAG 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   361 TGCCAGCCGTGCCCCCAGGATACCTTTCAGCCAGCAGCTTCAGAGCGTGCCAG 420

Qy   1 GTGGCAGAAACACCCACCTACCCCTGGCGGACGAGACAGGGAGCGCTGGTGTGC 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   88 GTGGCAGAAACACCCACCTACCCCTGGCGGACGAGACAGGGAGCGCTGGTGTGC 147

Qy   61 GCCCAGTGCCCCCAGGCACCTTGTGCAGCGGCCGGTGCCCGGAGCAGCCCACGACG 120
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   148 GCCCAGTGCCCCCAGGCACCTTGTGCAGCGGCCGGTGCCCGGAGCAGCCCACGACG 207

Qy   121 TGTGGCCCGTGTCCACCGGCGCCACTACAGCAGTTCTGGAACTACCTGGAGGCGCTGGCCGC 180
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   208 TGTGGCCCGTGTCCACCGGCGCCACTACAGCAGTTCTGGAACTACCTGGAGGCGCTGGCCGC 267

Qy   181 TACTGCAACGTCTCCTTGTCCGGGGAGCGTGAGGAGGAGCCGGGCCTTGCCAGGCCACCGAC 240
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   268 TACTGCAACGTCTCCTTGTCCGGGGAGCGTGAGGAGGAGCCGGGCCTTGCCAGGCCACCGAC 327

Qy   241 AACCGTGCCTGCGCGTGCCGCACGCGGCTTGTCCGGGGCACGCTGGTTCTGCTTGGAGCGAC 300
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   328 AACCGTGCCTGCGCGTGCCGCACGCGGCTTGTCCGGGGCACGCTGGTTCTGCTTGGAGCGAC 387

Qy   301 GCATCGTGTCCACCTGGTGCCCGGCGGTGAGTTGCCCCCGGCAGAACACGGCAG 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   388 GCATCGTGTCCACCTGGTGCCCGGCGGTGAGTTGCCCCCGGCAGAACACGGCAG 447

Qy   361 TGCCAGCCGTGCCCCCAGGCACCTTCTCAGCCAGCAGCTTCAGAGCCTGCCCAT 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   448 TGCCAGCCGTGCCCCCAGGCACCTTCTCAGCCAGCAGCTTCAGAGCCTGCCCAT 507

Qy   421 CCCCACCGCAACTGACAGGGCCCTGGGCGTCGGCGCCTTCCTCCCTCCTCCCCAT 480
          |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   508 CCCCACCGCAACTGACAGGGCCCTGGGCGTCGGCGCCTTCCTCCCTCCTCCCCAT 567

Qy   481 GACACCCTGTGCACCAGCTGCACTGGCTTCCCCCTTCAGCACCCAGGGGTACCAGGAGCTGAG 540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   568 GACACCCTGTGCACCAGCTGCACTGGCTTCCCCCTTCAGCACCCAGGGGTACCAGGAGCTGAG 627

Qy   541 GAGTGTGAGCGTGCCGTCATCGACTTTGTGCGTTCCAGCACATCCCATCAGAGGCTG 600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   541 GAGTGTGAGCGTGCCGTCATCGACTTTGTGCGTTCCAGCACATCCCATCAGAGGCTG 600

Qy   601 CAGCGGCTGCTGCCAGGCCTGCGAGGCCCGGAGGCCGCCTCGGGACACCCAAGGGCGGGC 660
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   628 GAGTGTGAGCGTGCCGTCATCGACTTTGTGCGTTCCAGGACATCTTCCATCAGAGGCTG 687

Qy   661 CCCGTGGGCCTTGGAGCTGGAGCTGCGGGGCTGGGCGGGCTTCCCGGGGGCCCCAGGAC 720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   601 CAGCGGCTGCTGCCAGGCCTGCGAGGCCCGGAGGCCGCCTCGGGACACCCAAGGGCGGGC 660

Qy   721 GGGGCCGTGCTGGTGCGGGCTGCTGCAGGACGTCGGCCGTGGCCCAGGATGCCCGGGCTGGAG 780
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   688 CAGCGGCTGCTGCCAGGCCCTGAGGCCCGAGGGCCGCTCGGGACCACCCAAGGGCGGGC 747

Qy   781 CCGAGGGTCCGTGAGCCCCTCCCTCCCCGTGCAC 813
          ||||||||||||||||||||||||||||||||||
Db   661 CCCGTGGGCCTTGGAGCTGGAGCTGCGGGGCTGGGCGGGCTTCCCGGGGGCCCCAGGAC 720

Qy   813
Db   748 GGGGCCGTGCTGGTGCGGGCTGCTGCAGGACGTCGGCCGTGGCCCAGGATGCCCGGGCTGGAG 807

Qy   868 CCGAGGCGTCCGTGAGCCGCTTCCCTCCCCGTGCAC 900
          ||||||||||||||||||||||||||||||||||
Db   808 GGGGCCGTGCTGGTGCGGGCTGCTGCAGGACGTCGGCCGTGGCCCAGGATGCCCGGGCTGGAG 867

Qy   781 CCGAGGGTCCGTGAGCCCCTCCCTCCCCGTGCAC 813
Db   781 CCGAGGGTCCGTGAGCCCCTCCCTCCCCGTGCAC 813

Qy   868 CCGAGGCGTCCGTGAGCCGCTTCCCTCCCCGTGCAC 900
Db   868 CCGAGGCGTCCGTGAGCCGCTTCCCTCCCCGTGCAC 900

RESULT 11
AAF62705
ID AAF62705 standard; cDNA; 1055 BP.
XX
AC AAF62705;
XX
DT 02-MAY-2001 (first entry)
XX
DE Human NTR3 nucleotide sequence.
XX
KW Human; NTR3; tumour necrosis factor receptor; TNF receptor; anti-HIV;
KW antianaemic; immunosuppressive; antidiabetic; antiviral; antibacterial;
KW cytostatic; neuroprotective; antiinflammatory; anorectic; vasotropic;
KW antirheumatoid, antiarthritic; cerebroprotective; tuberculostatic;
KW anti-obesity agent; cancer; blood disorder; brain disorder; autoimmune disease;
KW infection; sg.

```
(ELII ) LILLY & CO ELI.

Cohen PJ, Posada JA, Wierda D;

WPI; 2000-475441/41.
P-PSDB; AAY96596.

Use of mature FLINT for treating e.g. acute respiratory distress
syndrome, ulcerative colitis or ischemic injury during organ
transplantation

Example 7; Fig 1A-B, 125pp; English.

Human FLINT (also known as osteoprotegrin ?) is a new tumour necrosis
factor receptor (TNFR) superfamily member, which binds FasL and LIGHT and
prevents FasL-Fas interaction. Mature FLINT (mFLINT) inhibits FasL-Fas
mediated apoptotic and pro-inflammatory activity. mFLINT is useful for
treating acute respiratory distress syndrome, treating or inhibiting
ulcerative colitis, inhibiting ischemic injury during organ
transplantation or for organ preservation during transplantation. mFLINT
can also be used to treat acute liver failure, inflammation of the liver,
abnormal (hepatocyte) apoptosis, sepsis, disorders associated with
inflammation, hepatitis, ischemia, hypercoagulation or reperfusion,
damage to a cardiac myocyte resulting from abnormal myocardial ischaemia,
Type I diabetes, cancer, damage to an innocent bystander tissue induced
by a chemotherapeutic or therapeutic irradiation, aplastic anaemia,
myelodysplasia syndromes and pancytopenic conditions.
```

```
Query Match        900 BP; 128 A; 324 C; 304 G; 144 T; 0 other;
Best Local Similarity   100.0%; Score 813; DB 21; Length 900;
Matches   813; Conservative   0; Indels   1e-145; Mismatches   0; Gaps   0;
```

```
Qy    1 GYGGCAGAAACACCCACCTACCCCTGGCGGGACCCAGAGACAGGGGAGCGGCTGGTGTGC 60
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   88 GTGGCAGAAACACCCACCTACCCCTGGCGGGACCCAGAGACAGGGGAGCGGCTGGTGTGC 147

Qy   61 GCCCAGTGGCCCCCAGGCGACCTTTGTGCAGCGGCCCGTGCGCGAGACAGCCCCACGACG 120
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  148 GCCCAGTGGCCCCCAGGCGACCTTTGTGCAGCGGCCCGTGCGCGAGACAGCCCCACGACG 207

Qy  121 TGTGGGCCCGTGTCACCGGCCGCCACTNCACGCCNGTTCTGGAACTACCTGGAGCGCTCGCGC 180
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  208 TGTGGGCCCGTGTCACCGGCCGCCACTNCACGCCNGTTCTGGAACTACCTGGAGCGCTCGCGC 267

Qy  181 TACTTGCAACGTCCTCTGCGGGGGCGGTGAGAGGAGGCACGGGGCTTGCCAAGGCACCCAC 240
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  268 TACTTGCAACGTCCTCTGCGGGGGCGGTGAGAGGAGGCACGGGGCTTGCCAAGGCACCCAC 327

Qy  241 AACCGTGCCGCGTACCGACAGCACAGGCGCACCGTGGTTCTGGTGCAGGCAC 300
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  328 AACCGTGCCGCGTACCGACAGCACAGGCGCACCGTGGTTCTGGTGCAGGCAC 387

Qy  301 GCATCGTGTCAACCTGGTGCCGGCGTGATTGCCCCCGGGCACCCCCAGCCAGAACACGCAG 360
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  388 GCATCGTGTCAACCTGGTGCCGGCGTGATTGCCCCCGGGCACCCCCAGCCAGAACACGCGG 447

Qy  361 TGCCAGCCGTGCCCCCCAGGCACCTTCTCAGCCAGCAGGTCCAGGAGCAGTGCCCAG 420
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  448 TGCCAGCCGTGCCCCCCAGGCACCTTCTCAGCCAGCAGGTCCAGGAGCAGTGCCCAG 507

Qy  421 CGGCCCCACAGTGCCACAGGACGCCTGGCCTCTGGTCCCAGGCACGCCTCGTTCCTCCCCAT 480
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  508 CCCCACCCAACTGCACGCCCCTGGCCTGGCCTCTGGTCCCAGGCACGCCTCGTTCCTCCCCAT 567

Qy  481 CACACCCTGTGCACCAGCTCGCACTGGCTTCCCCCCTCAGCACGCAGGGTACCAGGGAGCTGAG 540
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  568 GACACCCTGTGCACCAGCTCGCACTGGCTTCCCCCCTCAGCACGCAGGGTACCAGGAGCTGAG 627

Qy  541 GAGTGTGAGCGTGCCCGTCATCGACTTTGTGCGCTTTCCAGGACAKTCTTCCATCAAGAGGCTG 600
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  628 GAGTGTGAGCGTGCCCGTCATCGACTTTGTGCGCTTTCCAGGACAKTCTTCCATCAAGAGGCTG 687

Qy  601 CAGCGGCTGCTGCAGGCCCTCGAGGCCCCGGAGGCTGGGGTTCCGGACACCAAGGCGGGC 660
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  688 CAGCGGCTGCTGCAGGCCCTCGAGGCCCCGGAGGCTGGGGTTCCGACACCAACCAAGGGCGGGC 747

Qy  661 CCCCGGGCCTTGCCAGCTGAAGCTCGCTCGGCGGCTCACCGAGCTCCTGGGGGCGCAGGAC 720
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  740 CCCCGGGCCTTGCCAGCTGAAGCTCGGTCGGCGGCGCTCACCGAGCTCCTGGGGCGCAGGAC 807

Qy  721 GGGGGACGTTGCGGCTTGCTCGCAGCGGCCGGGTGGCCAGGATGCCCGGGCTGGAG 780
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  808 GGGGGCCGTTGCGGCTGCTCGCAGCGGCCGGGTGCCCCAGGATGCCCGGGCTGGAG 867

Qy  781 CCGGACGTCCCGGAGCGGCTTCCCCGTCGTCAC 813
        |||||||||||||||||||||||||||||||||
Db  868 CCGAGCGTCCGGAGCGGCGTTCCCCGTCGTCAC 900
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RESULT 10
AX223010
ID   AX223010 standard; DNA; 903 BP.
XX
AC   AX223010;
XX
DT   20-MAY-1999  (first entry)
XX
DE   Orphan receptor (HUMAN NTR-1) polypeptide encoding DNA.
XX
KW   HUMAN NTR-1; orphan receptor; osteoprotegerin; OPG; TNFR; human;
KW   tumour necrosis factor receptor; muscle disorder; bone mass; screening;
KW   muscle metabolism; binding agent; cognate ligand; ss.
XX
OS   Homo sapiens.
XX
PN   WO9907738-A2.
XX
PD   18-FEB-1999.
XX
PF   04-AUG-1998; 98WO-US16202.
XX
PR   06-AUG-1997; 97US-0054869.
XX
PA   (PROC ) PROCTER & GAMBLE CO.
PA   (RGSB-) REGENERON PHARM INC.
XX
PI   Masiakowski PJ, Morris J, Valenzuela DM;
XX
DR   WPI; 1999-167365/14.
DR   P-PSDB; AAW95082.
XX
PT   Novel orphan human receptor polypeptide and nucleic acid - useful as
PT   diagnostic reagents and for treatment of muscle disorders
XX
PS   Claim 2; Page 21; 23pp; English.
XX
CC   This DNA encodes a HUMAN NTR-1 polypeptide, a novel orphan receptor. The
CC   protein is related to osteoprotegerin (OPG) and to tumour necrosis factor
CC   receptor (TNFR). Host cells transformed with a vector comprising the
CC   HUMAN NTR-1 nucleic acid are used for the recombinant expression of the
CC   protein. HUMAN NTR-1 proteins and antibodies immuno specific for the
CC   protein are useful for diagnosis and treatment of humans and animals,
CC   especially muscle disorders, as the receptor is involved in regulation of
CC   bone mass and muscle metabolism. HUMAN NTR-1 receptors are also useful
CC   for screening for agonists and cognate ligands, which may be
CC   used to treat disorders associated with HUMAN NTR-1 imbalance.
XX
SQ   Sequence 903 BP; 129 A; 324 C; 305 G; 145 T; 0 other;
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Query Match        100.0%; Score 813; DB 20; Length 903;
Best Local Similarity   100.0%; Pred No. 1e-145;
Matches   813; Conservative   0; Mismatches   0; Indels   0; Gaps   0;
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